

J. Hines

1645

PH#8

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/147,052

DATE: 07/12/2000  
 TIME: 12:35:24

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ENTERED

3 <110> APPLICANT: SAITOH, Shuji  
 4 TSUZAKI, Yoshinari  
 5 YANAGIDA, Noboru  
 7 <120> TITLE OF INVENTION: NOVEL FUSED PROTEIN, GENE THEREFOR, RECOMBINANT VECTOR,  
 8 RECOMBINANT VIRUS, AND ITS USE  
 10 <130> FILE REFERENCE: 981167  
 12 <140> CURRENT APPLICATION NUMBER: 09/147,052  
 13 <141> CURRENT FILING DATE: 1999-04-05  
 15 <150> PRIOR APPLICATION NUMBER: JP 08-103548  
 16 <151> PRIOR FILING DATE: 1996-03-29  
 18 <150> PRIOR APPLICATION NUMBER: PCT/JP97/01084  
 19 <151> PRIOR FILING DATE: 1997-03-28  
 21 <160> NUMBER OF SEQ ID NOS: 9  
 23 <170> SOFTWARE: PatentIn Ver. 2.1  
 25 <210> SEQ ID NO: 1  
 26 <211> LENGTH: 1371  
 27 <212> TYPE: DNA  
 28 <213> ORGANISM: hybrid  
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 33 gaggaagagt ctacgtttta tctttgtccc ccaccagtgg gttcaaccgt gatccgtcta 180  
 34 gaattcggct gtatgtctat tactaaaaaa gatgcaaacc caaataatgg ccaaacccaa 240  
 35 ttagaagcag cgcgaatgga gttaacagat ctaatcaatg ctaaagcgat gacattagct 300  
 36 tcactacaag actatgccaa gattgaagct agtttatcat ctgcttatag tgaagctgaa 360  
 37 acagttaaca ataaccctaa tgcaacatta gaacaactaa aaatggctaa aactaattta 420  
 38 gaatcagcca tcaaccaagc taatacggat aaaacgactt ttgataatga acacccaaat 480  
 39 ttagtgaag catacaaaagc actaaaaacc actttagaac aacgtgctac taaccttgaa 540  
 40 ggtttgtcat caactgctta taatcaaatt cgcaataatt tagtggatct atacaataaa 600  
 41 gctagtagtt taataactaa aacactagat ccactaaatg ggggaacgct ttagattctt 660  
 42 aatgagatta ctacagctaa taagaatatt aataatacgt tatcaactat taatgaacaa 720  
 43 aagactaatg ctgatgcatt atctaatagt tttattaaaa aagtgattca aaataatgaa 780  
 44 caaagttttg tagggacttt tacaaaacgt aatgttcaac cttcaaacta cagttttggt 840  
 45 gcttttagtg ctgatgtaac acccgtaaat tataaatatg caagaaggac cgtttggaat 900  
 46 ggtgatgaac cttcaagtag aattcttgca aacacgaata gtatcacaga tgtttcttgg 960  
 47 atttatagtt tagctggaac aaacacgaag taccatttta gttttagcaa ctatgggtcca 1020  
 48 tcaactgggt atttatattt cccttataag ttggttaaag cagctgatgc taataacggt 1080  
 49 ggattacaat acaaaattaaa taatggaaat gttcaacaag ttgagtttgc cacttcaact 1140  
 50 agtgcaaata atactacagc taatccaaact ccagcagttg atgagattaa agttgctaaa 1200  
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 52 gaaggaaata tgaataaagt tgcgccaatg attggcaaca tttatcttag ctcaaatgaa 1320  
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65 Tyr Gly Thr Asn Ser Ser Pro Ser Thr Gln Asn Val Thr Ser Arg Glu
66           20           25           30
68 Val Val Ser Ser Val Gln Leu Ser Glu Glu Glu Ser Thr Phe Tyr Leu
69           35           40           45
71 Cys Pro Pro Pro Val Gly Ser Thr Val Ile Arg Leu Glu Phe Gly Cys
72   50           55           60
74 Met Ser Ile Thr Lys Lys Asp Ala Asn Pro Asn Asn Gly Gln Thr Gln
75 65           70           75           80
77 Leu Glu Ala Ala Arg Met Glu Leu Thr Asp Leu Ile Asn Ala Lys Ala
78           85           90           95
80 Met Thr Leu Ala Ser Leu Gln Asp Tyr Ala Lys Ile Glu Ala Ser Leu
81           100          105          110
83 Ser Ser Ala Tyr Ser Glu Ala Glu Thr Val Asn Asn Asn Leu Asn Ala
84           115          120          125
86 Thr Leu Glu Gln Leu Lys Met Ala Lys Thr Asn Leu Glu Ser Ala Ile
87           130          135          140
89 Asn Gln Ala Asn Thr Asp Lys Thr Thr Phe Asp Asn Glu His Pro Asn
90 145          150          155          160
92 Leu Val Glu Ala Tyr Lys Ala Leu Lys Thr Thr Leu Glu Gln Arg Ala
93           165          170          175
95 Thr Asn Leu Glu Gly Leu Ser Ser Thr Ala Tyr Asn Gln Ile Arg Asn
96           180          185          190
98 Asn Leu Val Asp Leu Tyr Asn Lys Ala Ser Ser Leu Ile Thr Lys Thr
99           195          200          205
101 Leu Asp Pro Leu Asn Gly Gly Thr Leu Leu Asp Ser Asn Glu Ile Thr
102           210          215          220
104 Thr Ala Asn Lys Asn Ile Asn Asn Thr Leu Ser Thr Ile Asn Glu Gln
105 225          230          235          240
107 Lys Thr Asn Ala Asp Ala Leu Ser Asn Ser Phe Ile Lys Lys Val Ile
108           245          250          255
110 Gln Asn Asn Glu Gln Ser Phe Val Gly Thr Phe Thr Asn Ala Asn Val
111           260          265          270
113 Gln Pro Ser Asn Tyr Ser Phe Val Ala Phe Ser Ala Asp Val Thr Pro
114           275          280          285
116 Val Asn Tyr Lys Tyr Ala Arg Arg Thr Val Trp Asn Gly Asp Glu Pro
117           290          295          300
119 Ser Ser Arg Ile Leu Ala Asn Thr Asn Ser Ile Thr Asp Val Ser Trp
120 305          310          315          320
122 Ile Tyr Ser Leu Ala Gly Thr Asn Thr Lys Tyr Gln Phe Ser Phe Ser
123           325          330          335
125 Asn Tyr Gly Pro Ser Thr Gly Tyr Leu Tyr Phe Pro Tyr Lys Leu Val
126           340          345          350
128 Lys Ala Ala Asp Ala Asn Asn Val Gly Leu Gln Tyr Lys Leu Asn Asn
129           355          360          365
131 Gly Asn Val Gln Gln Val Glu Phe Ala Thr Ser Thr Ser Ala Asn Asn
132           370          375          380
134 Thr Thr Ala Asn Pro Thr Pro Ala Val Asp Glu Ile Lys Val Ala Lys

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138                               405                               410                               415
140 Val Pro Thr Gly Glu Gly Asn Met Asn Lys Val Ala Pro Met Ile Gly
141                               420                               425                               430
143 Asn Ile Tyr Leu Ser Ser Asn Glu Asn Asn Ala Asp Lys Ile Pro Gly
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152 <212> TYPE: DNA
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158 gaggaagagt ctacgtttta tctttgtccc ccaccagtgg gttcaaccgt gatccgtcta 180
159 gaaccgcccgc gaaaatgtcc cgaacctaga aaagccaccg agtggggtga aggaatcgcg 240
160 atattattta aagagaatat cagtccatat aaatttaaag tgacgcttta ttataaaaaat 300
161 atcattcaga cgacgacatg gacggggacg acatatagac agatcactaa tcgatataca 360
162 gataggacgc ccgttttccat tgaagagatc acggatctaa tcgacggcaa aggaagatgc 420
163 tcattctaaag caagatacct tagaacaat gtatatgttg aagcgtttga cagggatgcg 480
164 ggagaaaaaac aagtacttct aaaacctca aaattcaaca cgcgccgaatc tagggcatgg 540
165 cacacgacta atgagacgta taccgtgttg ggatcaccat ggatatatcg aacgggaacc 600
166 tccgtcaatt gtatagtaga ggaatggat gcccgcctcg tgtttccgta ttcatttttt 660
167 gcaatggcca atggcgacat cgcgaaacata tctccatttt atggtctatc cccaccagag 720
168 gctgcccgcg aacctatggg atatcccag gataatttca aacaactaga tagctatttt 780
169 tcaatggatt tggacaagcg tcgaaaagca agccttccag tcaagcgtaa ctttctcacc 840
170 acatcacact tcacagtgtg gtgggactgg gctccaaaaa ctactcgtgt atgttcaatg 900
171 actaagtgga aagaggtgac tgaatgttg cgtgcaacag ttaatgggag atacagattt 960
172 atggcccgtg aacttttcgc aacgtttatc agtaatacga ctgagtttga tccaaatcgc 1020
173 atcatattag gacaatgtat taaacgcgag gcagaagcag caatcgagca gatatttagg 1080
174 acaaaatata atgacagtca cgtcaaggtt ggacatgtac aatattttctt ggctctcggg 1140
175 ggatttattg tagcatatca gcctgttcta tccaaatccc tggctcataat gtacctcaga 1200
176 gaattgatga gagacaacag gaccgatgag atgctcgacc tggtaaacaa taagcatgca 1260
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186 ggatccggtt atgctttatt tgaaaactat aattttgtta agatggtaga cgtgcggat 1860
187 atacagattg ctagecattt tgtcgagctt aatctaacco tgctagaaga tcgggaaatt 1920
188 ttgcctttat ccgtttacac aaaagaagag ttgcgtgatg ttggtgtatt ggattatgca 1980
189 gaagtagctc gccgcaatca actacatgaa cttaaatttt atgacataaa caaagtaata 2040
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193 agtttatcat ctgcttatag tgaagctgaa acagttaaca ataaccttaa tgcaacatta 2280
194 gaacaactaa aaatggctaa aactaattta gaatcagcca tcaaccaagc taatacggat 2340
195 aaaacgactt ttgataatga acacccaaat ttagttgaag catacaaaagc actaaaaacc 2400
196 actttagaac aacgtgctac taaccttgaa ggtttgcat caactgctta taatcaaatt 2460
197 cgcaataatt tagtgatct atacaataaa gctagtagtt taataactaa aacactagat 2520
198 ccactaaatg ggggaacgct tttagattct aatgagatta ctacagctaa taagaatatt 2580
199 aataaacgt tatcaactat taatgaacaa aagactaatg ctgatgcatt atctaatagt 2640
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203 aacacgaata gtatcacaga tgtttcttgg atttatagtt tagctggaac aaacacgaag 2880
204 taccatttta gttttagcaa ctatggtcca tcaactgggt atttatattt cccttataag 2940
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206 gttcaacaag ttgagtttgc cacttcaact agtgcaata atactacagc taatccaact 3060
207 ccagcagttg atgagattaa agttgctaaa atcgttttat cagggtttaag atttgccaa 3120
208 aacacaatcg aattaagtgt tccaacgggt gaaggaaata tgaataaagt tgcgccaatg 3180
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214 <211> LENGTH: 1086
215 <212> TYPE: PRT
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223 20 25 30
225 Val Val Ser Ser Val Gln Leu Ser Glu Glu Glu Ser Thr Phe Tyr Leu
226 35 40 45
228 Cys Pro Pro Pro Val Gly Ser Thr Val Ile Arg Leu Glu Pro Pro Arg
229 50 55 60
231 Lys Cys Pro Glu Pro Arg Lys Ala Thr Glu Trp Gly Glu Gly Ile Ala
232 65 70 75 80
234 Ile Leu Phe Lys Glu Asn Ile Ser Pro Tyr Lys Phe Lys Val Thr Leu
235 85 90 95
237 Tyr Tyr Lys Asn Ile Ile Gln Thr Thr Thr Trp Thr Gly Thr Thr Tyr
238 100 105 110
240 Arg Gln Ile Thr Asn Arg Tyr Thr Asp Arg Thr Pro Val Ser Ile Glu
241 115 120 125
243 Glu Ile Thr Asp Leu Ile Asp Gly Lys Gly Arg Cys Ser Ser Lys Ala
244 130 135 140
246 Arg Tyr Leu Arg Asn Asn Val Tyr Val Glu Ala Phe Asp Arg Asp Ala
247 145 150 155 160
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250 165 170 175
252 Ser Arg Ala Trp His Thr Thr Asn Glu Thr Tyr Thr Val Trp Gly Ser
253 180 185 190

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259      210      215      220
261 Gly Asp Ile Ala Asn Ile Ser Pro Phe Tyr Gly Leu Ser Pro Pro Glu
262 225      230      235      240
264 Ala Ala Ala Glu Pro Met Gly Tyr Pro Gln Asp Asn Phe Lys Gln Leu
265      245      250      255
267 Asp Ser Tyr Phe Ser Met Asp Leu Asp Lys Arg Arg Lys Ala Ser Leu
268      260      265      270
270 Pro Val Lys Arg Asn Phe Leu Ile Thr Ser His Phe Thr Val Gly Trp
271      275      280      285
273 Asp Trp Ala Pro Lys Thr Thr Arg Val Cys Ser Met Thr Lys Trp Lys
274      290      295      300
276 Glu Val Thr Glu Met Leu Arg Ala Thr Val Asn Gly Arg Tyr Arg Phe
277 305      310      315      320
279 Met Ala Arg Glu Leu Ser Ala Thr Phe Ile Ser Asn Thr Thr Glu Phe
280      325      330      335
282 Asp Pro Asn Arg Ile Ile Leu Gly Gln Cys Ile Lys Arg Glu Ala Glu
283      340      345      350
285 Ala Ala Ile Glu Gln Ile Phe Arg Thr Lys Tyr Asn Asp Ser His Val
286      355      360      365
288 Lys Val Gly His Val Gln Tyr Phe Leu Ala Leu Gly Phe Ile Val
289      370      375      380
291 Ala Tyr Gln Pro Val Leu Ser Lys Ser Leu Ala His Met Tyr Leu Arg
292 385      390      395      400
294 Glu Leu Met Arg Asp Asn Arg Thr Asp Glu Met Leu Asp Leu Val Asn
295      405      410      415
297 Asn Lys His Ala Ile Tyr Lys Lys Asn Ala Thr Ser Leu Ser Arg Leu
298      420      425      430
300 Arg Arg Asp Ile Arg Asn Ala Pro Asn Arg Lys Ile Thr Leu Asp Asp
301      435      440      445
303 Thr Thr Ala Ile Lys Ser Thr Ser Ser Val Gln Phe Ala Met Leu Gln
304      450      455      460
306 Phe Leu Tyr Asp His Ile Gln Thr His Ile Asn Asp Met Phe Ser Arg
307 465      470      475      480
309 Ile Ala Thr Ala Trp Cys Glu Leu Gln Asn Arg Glu Leu Val Leu Trp
310      485      490      495
312 His Glu Gly Ile Lys Ile Asn Pro Ser Ala Thr Ala Ser Ala Thr Leu
313      500      505      510
315 Gly Arg Arg Val Ala Ala Lys Met Leu Gly Asp Val Ala Ala Val Ser
316      515      520      525
318 Ser Cys Thr Ala Ile Asp Ala Glu Ser Val Thr Leu Gln Asn Ser Met
319      530      535      540
321 Arg Val Ile Thr Ser Thr Asn Thr Cys Tyr Ser Arg Pro Leu Val Leu
322 545      550      555      560
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